Please amend the above-identified application as follows:

In the Claims:

1. (Currently Amended) A method of establishing a ~~genomic action map and/or~~ proteomic interaction map for comparison of pathophysiological and physiological processes comprising the steps of

(a) determining ~~genomic actions and/or~~ proteomic interactions for the pathophysiological process in the presence of simulated redox state perturbation(s) that is characteristic of [and specific to] the pathophysiological process;

(b) determining ~~genomic actions and/or~~ proteomic interactions for the physiological process in the presence of redox state that is associated with the physiological process;

(c) generating ~~an interaction~~ the proteomic map ~~from the determination of (a) that is more closely correlated with the pathophysiological process than if the determination of (a) were not carried out in the presence of simulated redox state perturbation(s) that is characteristic of and specific to the pathophysiological process, and from the determination of (b) that is more closely correlated with the physiological process than if the determination of (b) were not carried out in the presence of redox state that is associated with the physiological process~~ by identifying different proteomic interactions between (a) and (b).

2. (Currently Amended) The method of Claim 1 further comprising comparison of the ~~genomic actions and/or~~ proteomic interactions determined in (a) and the ~~genomic and/or~~ proteomic interactions determined in (b) to determine ~~genomic actions and/or~~ proteomic interactions that are causally related to the pathophysiological process.

3. (Currently Amended) A method of identifying target proteins ~~and/or genes~~ related to a disease comprising challenging cells involved in the disease with agent(s) to produce and identify redox state-related modifications of proteins and/or lipids that would subsequently mediate protein modification or that are characteristic of the disease.

4. (Original) The method of Claim 3 where the agent(s) constitute at least one redox state modifier molecule which is generated *in vivo* in the disease and affects the redox state of the cells in the disease and the modifications are protein-protein interactions obtained in response to the presence of the at least one redox state modifier molecule.

5. (Original) A method of correlating protein interaction(s) with oxygen tension comprising determining protein interaction(s) in the presence of an oxygen tension different from that in room air.

6. (Original) The method of Claim 5 where any set of proteins are employed in the determination, which are associated with a physiological process or a pathophysiological process.

7. (Original) The method of Claim 5 where a plurality of determinations are made with different oxygen tensions being employed in each determination.

8. (Original) The method of claim 5 where the oxygen tensions employed are in increments of 5 or 10 mm Hg.

9. (Original) The method of Claim 6 where the set of proteins is associated with a physiological process and the method is used to identify normal protein functions.

10. (Original) The method of Claim 6 where the set of proteins is associated with a pathophysiological process and the method is used to identify protein functions associated 'with the pathophysiological process.

11. (Original) A method of identifying previously unknown receptor or orphan receptor or activating ligand therefor comprising the step of measuring activation of receptor or orphan receptor in the presence of alteration of redox state.

12. (Original) A method of determining epitopes involved in and/or representing marker of disease comprising immunolabeling affected tissue or cells under redox conditions that are characteristic of the disease.